

Steven M. Ruben
Appl. No. 10/662,429

Human Genome Sciences, Inc.
Project Worksheet
HGS tumor necrosis factor (TNF-alpha)

Fri, Dec 3, 1999
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Project Information

Project Name	tumor necrosis factor (TNF-alpha)
Project Code	
Project Status	Active
HGS Code	25750
Clone ID	HTPAN08
Library	Human Pancreas Tumor
Patent Status	
PTO Serial #	
Created By	Ann Kim
Date Created	2/8/94
Date Modified	2/8/94

General Comments

HGS FULL LENGTH PROJECTS

HGS #: DATE:

CLONE DESIGNATION:

TISSUE SOURCE:

SB PROJECT #(if any):

GENE MATCH:

HGS SCIENTIST(S):

POTENTIAL MEDICAL APPLICATION:

BASIC RESEARCH APPLICATION:

POTENTIAL PHARMACEUTICAL COLLABORATORS:

POTENTIAL ACADEMIC COLLABORATORS:

PATENT INFORMATION:

RESULTS (Dated)

NUCLEOTIDE BLAST ANALYSIS:

PROTEIN BLAST ANALYSIS:

Query= HTPAN08R
(568 letters)

Translating both strands of query sequence in all 6 reading frames

Ruben EXHIBIT #98



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Project Information

Project Name tumor necrosis factor (TNF-alpha)
Project Code
Project Status Active
HGS Code 25750
Clone ID HTPAN08
Library Human Pancreas Tumor
Patent Status
PTO Serial #
Created By Ann Kim
Date Created 2/8/94
Date Modified 2/8/94

General Comments

HGS FULL LENGTH PROJECTS

HGS #: DATE:

CLONE DESIGNATION:

TISSUE SOURCE:

SB PROJECT #(if any):

GENE MATCH:

HGS SCIENTIST(S):

POTENTIAL MEDICAL APPLICATION:

BASIC RESEARCH APPLICATION:

POTENTIAL PHARMACEUTICAL COLLABORATORS:

POTENTIAL ACADEMIC COLLABORATORS:

PATENT INFORMATION:

RESULTS (Dated)

NUCLEOTIDE BLAST ANALYSIS:

PROTEIN BLAST ANALYSIS:

Query= HTPAN08R
 (568 letters)

Translating both strands of query sequence in all 6 reading frames

Ruben EXHIBIT 2098
Ruben v. Wiley et al.
Interference No. 105,077
RX 2098

**HGS**

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Database: nr
107,605 sequences; 30,094,510 total letters.
Searching.....done

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Poisson Probability P(N)	N
gp U03470 RNU03470_1 ligand for Fas antigen [Rattus n...	+1	84	0.00093	1
gp X01394 HSTNFR_3 Human mRNA for tumor necrosis fa...	+1	74	0.021	1
gp M30964 SYNHUMINF_1 Synthetic human tumor necrosis f...	+1	74	0.021	1
gp L09754 MUSCD30_1 CD30 antigen [Mus musculus]	+1	52	0.024	2
gp X02910 HSTNFA_1 TNF-alpha [Homo sapiens] >gp Z15...	+1	74	0.025	1
gp M10988 HUMINFAA_1 TNFA gene product [Homo sapiens]...	+1	74	0.025	1
gp X62141 PSPINF_1 tumor necrosis factor [Papio sp....	+1	74	0.025	1
gp M35592 SYNINFTRP_1 Synthetic human tumor necrosis f...	+1	74	0.025	1
gp M29079 PIGINFA_1 Porcine tumor necrosis factor al...	+1	72	0.045	1
gp L19123 RATTNFA_1 tumor necrosis factor-alpha [Rat...	+1	72	0.048	1

WARNING: Descriptions of 71 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (39.4 bits), Expect = 0.00093, P = 0.00093
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 226 GHSFLSNLHLRNGELVIHEKGFYYIYSQIYFRFQ 327
G + +S + + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197

Score = 53 (24.9 bits), Expect = 0.0021, Poisson P(2) = 0.0021
Identities = 10/29 (34%), Positives = 17/29 (58%), Frame = +1

Query: 394 YFGPILLMKSARIWGLKMQIWXYSTIKG 480
YFG ++LM+ ++ QIW +S+ G
Sbjct: 215 YPGDLVIMEEKKLNYCTTGQIWAHSSYLG 243

>gp|X01394|HSTNFR_3 Human mRNA for tumor necrosis factor [Homo sapiens]
Length = 157

Plus Strand HSPs:



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Score = 74 (34.7 bits), Expect = 0.021, P = 0.021
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +1

Query: 208 WESSRSGHSFSLNHLRNGELVIHEKGFYYTYSQTYFRFQ 327
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 28 WLNRRANALLANGVELRDNQLVWPSEGLYLIYSQVLFKGQ 67

>gp|M30964|SYNHUMINF_1 Synthetic human tumor necrosis factor (TNF) gene,
complete cds. [Artificial gene] >gp|A00362|A00362_1 tumor necrosis
factor alpha [None]
Length = 158

Plus Strand HSPs:

Score = 74 (34.7 bits), Expect = 0.022, P = 0.021
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +1

Query: 208 WESSRSGHSFSLNHLRNGELVIHEKGFYYTYSQTYFRFQ 327
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 29 WLNRRANALLANGVELRDNQLVWPSEGLYLIYSQVLFKGQ 68

SECOND WALK PROTEIN BLAST:

Query= HTPAN08Rp01
(342 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
107,605 sequences; 30,094,510 total letters.
Searching.....done

			Reading	High	Smallest	
			Frame	Score	Poisson	
Sequences producing High-scoring Segment Pairs:					Probability	
					P(N)	N
gp L11015 HUMLYTOXBA_1	lymphotoxin-beta [Homo sapiens]...	+1	78	0.0019	1	
gp X64387 VCHAG_2	haemagglutinin associated prote...	+1	46	0.022	2	
pir S25359 S25359	hypothetical protein YKL525 - y...	+1	42	0.20	3	
gp X64097 VCRVC_7	V.cholerae DNA for RVC repeated...	+2	44	0.60	2	
pir S15111 S15111	Hemorrhagic factor LHFII - Bush...	+1	38	0.76	2	
gp X56015 MICOENNR_2	NADH dehydrogenase subunit 4 [M...	-1	40	0.77	2	
gp M69077 PRDCG_13	Bacteriophage PRD1, complete ge...	-1	39	0.77	2	
gp M33581 MUSMDR1A_1	Mouse P-glycoprotein (mdrla) mR...	+1	40	0.78	3	
gp M30697 MUSMDRAA_1	Mouse multidrug resistance prot...	+1	40	0.78	3	
gp X14828 CHINFA_1	Goat mRNA for tumour necrosis f...	+1	58	0.85	1	
pir S06192 S06192	tumor necrosis factor alpha pre...	+1	58	0.85	1	



gp M22647 PIGAPOB02_1	Pig apolipoprotein B gene (Lpb)...	+2	36	0.89	3
gp X03614 PAMFHN1_1	Sendai virus (strain Z) genome ...	-1	55	0.91	1
gp L19357 CRULGPB_1	lysosomal membrane glycoprotein...	-2	54	0.92	1
gp M97501 HUMCLIP_1	cytoplasmic linker protein-170 ...	+1	41	0.93	2
gp X64838 HSRESTIN_1	restin [Homo sapiens] >pir S226...	+1	41	0.94	2
pir S13421 S13421	Globin - Brine shrimp 0.0 0.0...	-1	36	0.95	3
pir JT0382 JT0382	apolipoprotein B - pig (fragmen...	+2	36	0.95	3
gp M35105 RATCROS1B_1	Rat lung-derived L01 c-ros-1 pr...	+1	38	0.96	3
gp X58886 SVLARGEP_2	reverse peptide [Sendai virus]	-1	54	0.97	1

WARNING: Descriptions of 2 database sequences were not reported due to the limiting value of parameter V = 20.

```
>gp|L11015|HUMLYTOXBA_1 lymphotoxin-beta [Homo sapiens] >gp|L11016|HUMLYTOXBB_1
  lymphotoxin-beta [Homo sapiens] >pir|A46066|A46066 lymphotoxin beta
  - human | 0.0 0.0 0.0 0.0 0.0
  Length = 244
```

Plus Strand HSPs:

Score = 78 (37.6 bits), Expect = 0.0019, P = 0.0019
Identities = 12/37 (32%), Positives = 25/37 (67%), Frame = +1

```
Query: 151 GGIXELKENDRILVSVINEHLIDMDHEASFFGAFLVG 261
      GG+ +L+ +R+ V++++ ++D +FFGA +VG
Sbjct: 208 GGLVQLRRGERVYVNLSHPDMVDFARGKTFFGAVMVG 244
```

LENGTH OF CLONE(nucleotides):
PREDICTED LENGTH OF FULL LENGTH:
METHOD TO OBTAIN FULL LENGTH:
TISSUE DISTRIBUTION (alternate splicing?):

PROTEIN EXPRESSION:

FUNCTIONAL STUDIES (completed and planned):

TERMINATION (REASON):

Protein BLAST Analysis

Protein BLAST of the Reverse sequence

Smallest



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Sequences producing High-scoring Segment Pairs:			Reading Frame	High Score	Poisson Probability P(N)	N
gp U03470	RNU03470_1	ligand for Fas antigen [Rattus n...	+2	85	0.00028	1
gp S52010	S52010_2	orf1 5' of EpoR, orf2 5' of EpoR...	-3	45	0.18	2
gp X01394	HSTNFR_3	Human mRNA for tumor necrosis fa...	+2	65	0.21	1
gp M30964	SYNHUMINF_1	Synthetic human tumor necrosis f...	+2	65	0.21	1
gp X02910	HSTNFA_1	TNF-alpha [Homo sapiens] >gp Z15...	+2	65	0.23	1
gp M10988	HUMINFAA_1	TNFA gene product [Homo sapiens]...	+2	65	0.23	1
gp X62141	PSPINF_1	tumor necrosis factor [Papio sp....	+2	65	0.23	1
gp M35592	SYNINFTRP_1	Synthetic human tumor necrosis f...	+2	65	0.23	1
pir C21124	C21124	Bkm-like sex-determining region ...	-1	39	0.49	2
gp K01664	DRORSXA_1	D.melanogaster Bkm-like DNA (pro...	-1	39	0.49	2

WARNING: Descriptions of 28 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 85 (39.4 bits), Expect = 0.00028, P = 0.00028
Identities = 15/34 (44%), Positives = 22/34 (64%), Frame = +2

Query: 86 GNXFSLNLHLRNGELVIHEKGFYYTYSQTYFRFQ 187
G +S + + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197

Protein BLAST of the CONTIG containing reverse sequence and second and third walks

Sequences producing High-scoring Segment Pairs:			Frame	Score	P(N)	N
gp U03470	RNU03470_1	ligand for Fas antigen [Rattus n...	+2	84	0.00029	1
gp X01394	HSTNFR_3	Human mRNA for tumor necrosis fa...	+2	74	0.0085	1
gp M30964	SYNHUMINF_1	Synthetic human tumor necrosis f...	+2	74	0.0086	1
gp X02910	HSTNFA_1	TNF-alpha [Homo sapiens] >gp Z15...	+2	74	0.0098	1
gp M10988	HUMINFAA_1	TNFA gene product [Homo sapiens]...	+2	74	0.0098	1
gp X62141	PSPINF_1	tumor necrosis factor [Papio sp....	+2	74	0.0098	1
gp M35592	SYNINFTRP_1	Synthetic human tumor necrosis f...	+2	74	0.0098	1
gp M35027	VACCG_237	Vaccinia virus, complete genome....	-2	46	0.011	2
gp M29079	PIGINFA_1	Porcine tumor necrosis factor al...	+2	72	0.019	1
gp L19123	RATTNFA_1	tumor necrosis factor-alpha [Rat...	+2	72	0.020	1



WARNING: Descriptions of 94 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNJ03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (42.3 bits), Expect = 0.00029, P = 0.00029
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +2

Query: 179 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 280
G + +S + + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYYKGGVLVINEAGLYFVYSKVYFRGQ 197

>gp|X01394|HSTNFR_3 Human mRNA for tumor necrosis factor [Homo sapiens]
Length = 157

Plus Strand HSPs:

Score = 74 (37.3 bits), Expect = 0.0086, P = 0.0085
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +2

Query: 161 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 280
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 28 WLNRRANALLANGVELRDNLVVPSEGLYLIYSQVLFKGQ 67

>gp|M30964|SYNHUMINF_1 Synthetic human tumor necrosis factor (TNF) gene,
complete cds. [Artificial gene] >gp|A00362|A00362_1 tumor necrosis
factor alpha [None]
Length = 158

Plus Strand HSPs:

Score = 74 (37.3 bits), Expect = 0.0086, P = 0.0086
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +2

Query: 161 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 280
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 29 WLNRRANALLANGVELRDNLVVPSEGLYLIYSQVLFKGQ 68

Query= HTPAN08Rev + Walks+ Forward Sequences
(1198 letters)



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Translating both strands of query sequence in all 6 reading frames

Database: nr

113,553 sequences; 31,868,292 total letters.

Searching.....done

Sequences producing High-scoring Segment Pairs:			Reading Frame	High Score	Smallest Poisson Probability P(N)	N
pir S A40201	artifact-warning sequence (trans...	+1	241	2.7e-77	3	
pir S C40201	artifact-warning sequence (trans...	+3	246	1.3e-59	2	
pir S F40201	artifact-warning sequence (trans...	+1	180	1.0e-21	2	
pir S D40201	artifact-warning sequence (trans...	+1	81	2.1e-19	4	
gp X55777 HSMCHHS_2	H.sapiens Mahlavu hepatocellular...	+1	190	2.3e-19	1	
gp L27065 HUMNF2A_1	NF2 gene product [Homo sapiens]	-3	139	3.7e-14	1	
pir S E40201	artifact-warning sequence (trans...	+3	98	2.5e-12	4	
gp L20321 HUMSTK2A_1	protein serine/threonine kinase ...	-1	137	3.7e-12	1	
gp S58722 S58722_1	X-linked retinopathy protein {3'...	-1	128	1.8e-11	1	
pir S A46010	X-linked retinopathy protein (C-...	-1	128	1.8e-11	1	
gp M84237 HUMIGTB1A_2	integrin beta-1 subunit [Homo sa...	-3	116	9.6e-11	1	
pir S A42442	beta 1 integrin subunit, beta 1S...	-3	116	9.6e-11	1	
gp L24521 HUMTRRP_1	transformation-related protein [...	-3	120	9.7e-10	1	
gp L11672 HUMKRUPZN_1	zinc finger protein [Homo sapiens]	+2	108	6.1e-08	1	
gp U03470 RNU03470_1	ligand for Fas antigen [Rattus n...	+1	84	1.3e-06	2	
gp X14828 CHINFA_1	Goat mRNA for tumour necrosis fa...	+1	65	2.8e-06	2	
pir S S06192	tumor necrosis factor alpha prec...	+1	65	2.8e-06	2	
pir S B26359	decay-accelerating factor 2 prec...	-3	96	5.3e-06	1	
gp L26953 HUMPROTXA_1	Homo sapiens chromosomal protein...	+1	101	6.2e-06	1	
gp A06305 A06305_1	lymphotoxin [None]	+1	99	7.2e-06	1	
gp X77317 CHINFAMR_1	tumour necrosis factor alpha [Ca...	+1	63	7.8e-06	2	
pir S B32877	tumor necrosis factor beta precu...	+1	99	8.3e-06	1	
pir S S34742	lymphotoxin - human	+1	99	8.3e-06	1	
pir S S26951	tumor necrosis factor beta - human	+1	99	8.3e-06	1	
gp A00324 A00324_1	tumor necrosis factor beta [Arti...	+1	99	8.4e-06	1	

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (40.3 bits), Expect = 0.0017, P = 0.0017

Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 85 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 186

G + +S + + G LVI+E G Y++YS+ YFR Q

Subjct: 164 GTALISGVKYKKGGGLVINEAGLYFVYSKVYFRGQ 197



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Score = 66 (31.7 bits), Expect = 1.3e-06, Poisson P(2) = 1.3e-06
Identities = 12/39 (30%), Positives = 22/39 (56%), Frame = +1

Query: 325 YSTYQGGIFELKENDRILVSVINEHLIDMHEASFFGAF 441
+S Y G +F L D + V+++ LI+ + +FFG +
Sbjct: 238 HSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLY 276

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